

SEQUENCE LISTING

INS. A4 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2107
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGGAG ACTTTTTTTT GAAAGGAAAC TAGGGAGGGA GGGAGAGGGA	60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG	115
	Met 1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT	163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His	
5 10 15	
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA	211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr	
20 25 30	
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG	259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys	
35 40 45	
TAC GGC TAC CTT CCA CCG ACT AGC CCC AGA ATG TCA GTC GTG CGC TCT	307
Tyr Gly Tyr Leu Pro Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser	
50 55 60 65	
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC	355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly	
70 75 80	
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT CAC TGG ATG AAG	403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys	
85 90 95	
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT	451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe	
100 105 110	
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC	499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His	
115 120 125	

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AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC	547
Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp	
130 135 140 145	
CCT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT GTG TGG CAG AAT	595
Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn	
150 155 160	
GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT	643
Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn	
165 170 175	
GGC AAA CGT GAT GTG GAT ATA CCC ATT ATT TTT GCA TCT GGT TTC CAT	691
Gly Lys Arg Asp Val Asp Ile Pro Ile Ile Phe Ala Ser Gly Phe His	
180 185 190	
GGG GAC AGC TCT CCC TTT GAT GGA GAG GGA GGA TTT TTG GCA CAT GCC	739
Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His Ala	
195 200 205	
TAC TTC CCT GGA CCA GGA ATT GGA GGA GAT ACC CAT TTT GAC TCA GAT	787
Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser Asp	
210 215 220 225	
GAG CCA TGG ACA CTA GGA AAT CCT AAT CAT GAT GGA AAT GAC TTA TTT	835
Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe	
230 235 240	
CTT GTA GCA GTC CAT GAA CTG GGA CAT GCT CTG GGA TTG GAG CAT TCC	883
Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His Ser	
245 250 255	
AAT GAC CCC ACT GCC ATC ATG GCT CCA TTT TAC CAG TAC ATG GAA CAG	931
Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu Gln	
260 265 270	
ACA CTT CAA CTA CCT AAT GAT GAT TAC AGG CAT CAG AGA TAT ATG TCA	979
Thr Leu Gln Leu Pro Asn Asp Asp Tyr Arg His Gln Arg Tyr Met Ser	
275 280 285	
CCT GAC AAG ATT CCT CCA CCT ACA AGA CCT CTA CCG ACA GTG CCC CCA	1027
Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr Val Pro Pro	
290 295 300 305	
CAC CGC TCT ATT CCT CCG GCT GAC CCA AGG AAA AAT GAC AGG CCA AAA	1075
His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp Arg Pro Lys	
310 315 320	
CCT CCT CGG CCT CCA ACC GGC AGA CCC TCC TAT CCC GGA GCC AAA CCC	1123
Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly Ala Lys Pro	
325 330 335	
AAC ATC TGT GAT GGG AAC TTT AAC ACT CTA GCT ATT CTT CGT CGT GAG	1171
Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu Arg Arg Glu	
340 345 350	

ATG	TTT	GTT	TTC	AAG	GAC	CAG	TGG	TTT	TGG	CGA	GTG	AGA	AAC	AAC	AGG	1219
Met	Phe	Val	Phe	Lys	Asp	Gln	Trp	Phe	Trp	Arg	Val	Arg	Asn	Asn	Arg	
355						360					365					
GTG	ATG	GAT	GGA	TAC	CCA	ATG	CAA	ATT	ACT	TAC	TTC	TGG	CGG	GGC	TTG	1267
Val	Met	Asp	Gly	Tyr	Pro	Met	Gln	Ile	Thr	Tyr	Phe	Trp	Arg	Gly	Leu	
370					375					380					385	
CCT	CCT	AGT	ATC	GAT	GCA	GTT	TAT	GAA	AAT	AGC	GAC	GGG	AAT	TTT	GTG	1315
Pro	Pro	Ser	Ile	Asp	Ala	Val	Tyr	Glu	Asn	Ser	Asp	Gly	Asn	Phe	Val	
				390					395					400		
TTC	TTT	AAA	GGT	AAC	AAA	TAT	TGG	GTG	TTC	AAG	GAT	ACA	ACT	CTT	CAA	1363
Phe	Phe	Lys	Gly	Asn	Lys	Tyr	Trp	Val	Phe	Lys	Asp	Thr	Thr	Leu	Gln	
			405					410					415			
CCT	GGT	TAC	CCT	CAT	GAC	TTG	ATA	ACC	CTT	GGA	AGT	GGA	ATT	CCC	CCT	1411
Pro	Gly	Tyr	Pro	His	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Gly	Ile	Pro	Pro	
			420				425					430				
CAT	GGT	ATT	GAT	TCA	GCC	ATT	TGG	TGG	GAG	GAC	GTC	GGG	AAA	ACC	TAT	1459
His	Gly	Ile	Asp	Ser	Ala	Ile	Trp	Trp	Glu	Asp	Val	Gly	Lys	Thr	Tyr	
	435					440					445					
TTC	TTC	AAG	GGA	GAC	AGA	TAT	TGG	AGA	TAT	AGT	GAA	GAA	ATG	AAA	ACA	1507
Phe	Phe	Lys	Gly	Asp	Arg	Tyr	Trp	Arg	Tyr	Ser	Glu	Glu	Met	Lys	Thr	
450					455					460					465	
ATG	GAC	CCT	GGC	TAT	CCC	AAG	CCA	ATC	ACA	GTC	TGG	AAA	GGG	ATC	CCT	1555
Met	Asp	Pro	Gly	Tyr	Pro	Lys	Pro	Ile	Thr	Val	Trp	Lys	Gly	Ile	Pro	
				470					475					480		
GAA	TCT	CCT	CAG	GGA	GCA	TTT	GTA	CAC	AAA	GAA	AAT	GGC	TTT	ACG	TAT	1603
Glu	Ser	Pro	Gln	Gly	Ala	Phe	Val	His	Lys	Glu	Asn	Gly	Phe	Thr	Tyr	
			485					490					495			
TTC	TAC	AAG	GAA	GGA	GTA	TTG	GAA	ATT	CAA	ACA	ACC	AGA	TAC	TCA	AGG	1651
Phe	Tyr	Lys	Glu	Gly	Val	Leu	Glu	Ile	Gln	Thr	Thr	Arg	Tyr	Ser	Arg	
		500					505					510				
CTA	GAA	CCT	GGA	CAT	CCA	AGA	TCC	ATC	CTC	AAG	GAT	TTA	TCG	GGC	TGT	1699
Leu	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp	Leu	Ser	Gly	Cys	
	515					520					525					
GAT	GGA	CCA	ACA	GAC	AGA	GTT	AAA	GAA	GGA	CAC	AGC	CCA	CCA	GAT	GAT	1747
Asp	Gly	Pro	Thr	Asp	Arg	Val	Lys	Glu	Gly	His	Ser	Pro	Pro	Asp	Asp	
530					535					540					545	
GTA	GAC	ATT	GTC	ATC	AAA	CTG	GAC	AAC	ACA	GCC	AGC	ACT	GTG	AAA	GCC	1795
Val	Asp	Ile	Val	Ile	Lys	Leu	Asp	Asn	Thr	Ala	Ser	Thr	Val	Lys	Ala	
				550					555					560		
ATA	GCT	ATT	GTC	ATT	CCC	TGC	ATC	TTG	GCC							

Asp Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln
 145 150 155 160
 Asn Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu
 165 170 175
 Asn Gly Lys Arg Asp Val Asp Ile Pro Ile Ile Phe Ala Ser Gly Phe
 180 185 190
 His Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His
 195 200 205
 Ala Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser
 210 215 220
 Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu
 225 230 235 240
 Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His
 245 250 255
 Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu
 260 265 270
 Gln Thr Leu Gln Leu Pro Asn Asp Asp Tyr Arg His Gln Arg Tyr Met
 275 280 285
 Ser Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr Val Pro
 290 295 300
 Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp Arg Pro
 305 310 315 320
 Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly Ala Lys
 325 330 335
 Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu Arg Arg
 340 345 350
 Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg Asn Asn
 355 360 365
 Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp Arg Gly
 370 375 380
 Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly Asn Phe
 375 390 395 400
 Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp Thr Thr Leu
 405 410 415
 Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser Gly Ile Pro
 420 425 430
 Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val Gly Lys Thr
 435 440 445

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~~Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu Glu Met Lys
450 455 460
Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp Lys Gly Ile
455 470 475 480
Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn Gly Phe Thr
485 490 495
Tyr Phe Tyr Lys Glu Gly Val Leu Glu Ile Gln Thr Thr Arg Tyr Ser
500 505 510
Arg Leu Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp Leu Ser Gly
515 520 525
Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser Pro Pro Asp
530 535 540
Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser Thr Val Lys
545 550 555 560
Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu Leu Val
565 570 575
Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro Arg His
580 585 590
Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val
595 600 604~~

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

SGNVVNGCWG AYATMRTSAT

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

YTCRTSNTCR TCRAARTGRR HRTCYYCC

27

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp
1 5 10 14

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln
1 5 10 15

Ser Ala
18

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~~A4~~ (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

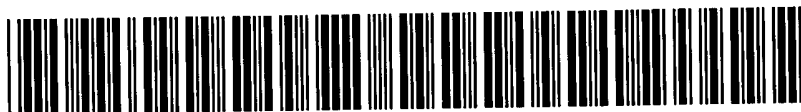
(A) LENGTH: 14
(B) TYPE: Amino acid
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu
1 5 10 14

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1	LET.	1
2	A...	1
3	SEQLIST	10

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